```
> O <
O | O    IntelliGenetics
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```

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file Seq140-aay87247.res made by tport on Wed 14 Jan 104 14:59:51-PST.

Query sequence being compared:US-10-006-485A-140 (1-311)
                               aay87247
Number of sequences searched: 1
Number of scores above cutoff: 1

Results of the initial comparison of US-10-006-485A-140 (1-311) with:
          File : aay87247.pep

SCORE	0	34	69	103	138	172	207	241	276	310
STDEV										

```
100-

N    -
U  50-
M    -
B    -
E    -
R    -

O 10-
F    -

S  5-
C    -
O    -
R    -
E    -
S  3-
    2-
    1-
    0-                                                    *
```

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig. Frame
1. aay87247	Human signal peptide containing protein HSPP-24 SE	311	310	310	0.00 0

1. US-10-006-485A-140 (1-311).   Human signal peptide containing protein HSPP-24 SE
   aay87247

Initial Score   = 310   Optimized Score   = 310   Significance = 0.00
Residue Identity   = 99%   Matches   = 309   Mismatches   =   1
Gaps   =   Conservative Substitutions   =   1

```
X         10        20        30        40        50        60        70
MGVPTALEAGSWRWGSLLFALFLAAASLGPVAAFKVATPYSLYVCPEGQNVTLTCRLLGPVDKGHDVTFYKTW
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
MGVPTAPEAGSWRWGSLLFALFLAAASLGPVAAFKVATPYSLYVCPEGQNVTLTCRLLGPVDKGHDVTFYKTW
X         10        20        30        40        50        60        70

          80        90       100       110       120       130       140
YRSRGEVQTCSERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLESASDHHGNFSITMRNLTLLDSGLY
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
YRSSRGEVQTCSERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLESASDHHGNFSITMRNLTLLDSGLY
          80        90       100       110       120       130       140

         150       160       170       180       190       200       210
CCLVEIRHHSEHRVHGAMELQVQTGKDAPSNCVVYPSSSQDSENITAAALATGACIVGILCLPLILLLVY
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CCLVEIRIHHSEHRVHGAMELQVQTGKDAPSNCVVYPSSSQBSENITAAALATGACIVGILCLPLILLLVY
         150       160       170       180       190       200       210

         220       230       240       250       260       270       280
KQRQAASNRRAQELVRMDSNIQGIENPGFEASPPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSP
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
KQRQAASNRRAQELVRMDSNIQGIENPGFEASPPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSP
         220       230       240       250       260       270       280

         290       300       X
PGPGDVFFPSLDPVPDSNPFEVI
|||||||||||||||||||||||
PGPGDVFFPSLDPVPDSNPFEVI
         290       300       310
```

PARAMETERS

Similarity matrix	PAM-150		
Threshold level of sim.	16%	K-tuple	1
Mismatch penalty	1		
Gap penalty	5.00	Joining penalty	20
Gap size penalty	0.05	Window size	311
Cutoff score	1		
Randomization group	0		

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	310	0	0.00

Times:	CPU	Total Elapsed
	00:00:00.00	00:00:00.00

Number of residues:	311
Number of sequences searched:	1
Number of scores above cutoff:	1

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is: